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GenCore version 5.1.3
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OM protein - nucleic search, using frame_plus_p2n model

Run on: November 9, 2002, 04:35:07 ; Search time 2784 Seconds

(without alignments)
1986.183 Million cell updates/sec

Title: US-09-895-298A-83

Perfect score: 1002

Sequence: 1 MMNFQPSKAMRASQMTFF.....HDGSLDLRRSRVQEGNRA 190

Scoring table:
BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 2054640 segs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-DB=genembl -QFMT=fastap -SUFFIX=rge -MINMATCH=0.1 -LOOFCI=0 -LOOPEXT=4
-UNITS=bits -START=1 -END=-1 -MATRIX=blsum62 -TRANS=humand4.cdi -LIST=45
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-WARN.TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -Fgapop=6 -Fgapext=7
-YGAPOP=10 -YGAPEXT=0.5 -DELop=6 -DElext=7

Database : GenEmbl:*
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41: em_htgo_other:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1002	100.0	1219	6	AX108540 Sequence
2	1002	100.0	1813	6	AX023655 Homo sapi
3	1002	100.0	1960	6	AX108538 Sequence
4	1002	100.0	2407	6	AX108534 Sequence
5	1002	100.0	2521	6	AX108536 Sequence
6	1002	100.0	2760	9	BC027602 Homo sapi
7	995	99.3	2387	9	AK093944 Homo sapi
8	680	67.9	2399	9	AK097718 Homo sapi
9	327	32.6	220633	9	HU091321 Human Chrom
10	327	32.6	223280	2	AC130456 Homo sapi
11	307	30.6	71596	2	AC100877 Mus muscu
12	293	29.2	1639	9	AB002405 Homo sapi
13	293	29.2	1804	9	BC018346 Homo sapi
14	293	29.2	5291	9	AK074065 Homo sapi
15	291.5	29.1	1848	10	BC004840 Mus muscu
16	290.5	29.0	1658	10	BC013502 Mus muscu
17	253.5	25.3	1983	10	BC005510 Mus muscu
18	253.5	25.3	2614	10	BC006956 Mus muscu
19	228.5	22.8	81704	9	AL512353 Human DNA
20	228.5	22.8	192180	2	AC023331 Homo sapi
21	226.5	22.6	110000	2	AC124444_2
22	212	21.2	402	6	AX071021 Sequence
23	195.5	19.5	164564	9	HDAC003108 Human Chr
24	184	18.4	623	10	AJ297000 Mus muscu
25	165.5	16.5	37026	9	CNS00YVF
26	165.5	16.5	177738	9	AC021593 Homo sapi
27	158	15.8	193465	2	AL645856 Mus muscu
28	118	11.8	2779	9	AK024893 Homo sapi
29	107.5	10.7	1633	6	AX464084 Sequence
30	105.5	10.5	168582	2	AC079534 Mus muscu
31	104.5	10.4	1803	9	BC016931 Homo sapi
32	104.5	10.4	2738	9	AF093239 Homo sapi
33	104.5	10.4	2771	9	AF398509 Homo sapi
34	103.5	10.3	175744	2	AC109189 Mus muscu
35	103	10.3	94212	2	AC091848 Homo sapi
36	103	10.3	210202	2	AC008778 Homo sapi
37	103	10.3	221452	9	AC034242 Homo sapi
38	102.5	10.2	201309	10	AL669857 Mouse DNA
39	101.5	10.1	185290	2	AL844560 Mus muscu
40	101	10.1	162004	2	AC110554 Mus muscu
41	101	10.1	171394	2	AC102779 Mus muscu
42	101	10.1	194374	2	AC016766 Homo sapi
43	100	10.0	71596	2	AC100877 Mus muscu
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45	99.5	9.9	3216	10	AF417581 Mus muscu

RESULT 1

ALIGNMENTS

AXI08540	AXI08540	1219 bp	DNA	linear	PAT 30-APR-2001
LOCATION	Sequence 7 from Patent WO0123417.				
DEFINITION	AXI08540				
ACCESSION	AXI08540.1	GI:13923839			
VERSION					
KEYWORDS	human.				
SOURCE	human.				
ORGANISM	Homo sapiens				
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
REFERENCE	1 (bases 1 to 1219)				
AUTHORS	vinals y de Bassols,C.				
TITLE	Human tumor-associated lak-4p related polynucleotides and				
	polypeptides and their uses				
JOURNAL	Patent: WO 0123417-A 7 05-APR-2001;				
	SMITHKLINE BEECHAM BIOLOGICALS S.A. (BE)				
FEATURES	Location/Qualifiers				
source	1..1219				
	/organism="Homo sapiens"				
	/db_xref="taxon:9606"				
BASE COUNT	346 a 260 c 275 g 338 t				
ORIGIN					
Alignment Scores:					
Pred. No.:	2,29e-102	Length:	1219		
Score:	1002.00	Matches:	190		
Percent Similarity:	100.00%	Conservative:	0		
Best Local Similarity:	100.00%	Mismatches:	0		
Query Match:	100.00%	Indels:	0		
DB:	6	Gaps:	0		
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QY	1 MetMetAsnPheGlnProProSerLysAlaTrpArgAlaSerGlnMetMetPhePhe	20			
DB	4 ATGATGATTTCCAGACCTCCGACGAAGCTCGCGGCTCAGACATGACTTTCTTC	63			
QY	21 IlePheLeuLeuPhePheProSerPheThrGlyValLeuCyThrLeuAlaIleThrIle	40			
DB	64 ATCTCTTGCTCTTTTCCCATCTTTCACGCGGGCTGTGCACCCGTGGCATCACCATC	123			
QY	41 TrpArgLeuLysProSerAlaAspCysGlyProPheArgGlyLeuProLeuPheIleHis	60			
DB	124 TGGGATTTGAAGCCTTCAGCTGACTGAGTGCGCTTTGCAAGGTCTGCTCTTCATTAC	183			
QY	61 SerIleYrSerTrpIleAspPThrLeuSerThrArgProGlyYrLeuTrpValValTrp	80			
DB	184 TCCATCTACAGCTGGATCGACACCCCTAAGTACAGCGCTGGCTACCTGGGTGTGG	243			
QY	81 IleYrTrArgAsnLeuIleGlySerValHisPhePhePheIleuThrLeuIleValLeu	100			
DB	244 ATCTATGTGGAACCTCATTTGGAAGTGTGACTCTTTTTCATCCCTCACCCCTATTGTGCTG	303			
QY	101 IleIleThrYrLeuYrYrTrpGlnIleThrGlnGlyArgYsIleMetIleArgLeuLeu	120			
DB	304 ATCATCAACCATCTTTACTGGCAGATCACAGAGGAAGAAAGATTATATAGAGCTGCTC	363			
QY	121 HisGlnGlnIleIleAsnGlnGlyLysAspLysMetPheLeuIleGluLysLeuIleLys	140			
DB	364 CATGACGAGATCATTAATGAGGCGAAGATTAATAATGTCTCGATGAGAAATTTGATCAAG	423			
QY	141 LeuGlnAspMetGlyLysLysAlaAsnProSerSerLeuValLeuGlnArgGluVal	160			
DB	424 CTGAGAGATATGGGAAGAAAGCAACCCAGCTCCTCTTGCGAAAGAGAGAGAGTG	483			
QY	161 GlnGlnGlnGlyPheLeuHisLeuGlyGlnHisAspGlySerLeuAspLeuArgSerArg	180			
DB	484 GAGCAACAAGGCTTTTTCGATTTTGGGGGACATATGATGCAATCTTGACTTGGCATCTAGA	543			
QY	181 ArgSerValGlnGlnGlyAsnProArgAla 190				
DB	544 AGATCACTTCAAGAAAGTAAATCCAAAGGCC 573				

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RESULT 2
AK023655      1813 bp      mRNA      linear      PRI 01-AUG-2002
DEFINITION   Homo sapiens CDNA FLJ13593 f1s, clone PLACE1009493.
ACCESSION    AK023655
VERSION      AK023655.1 GI:10435644
KEYWORDS     oligo capping; f1s (full insert sequence).
SOURCE       Homo sapiens placenta CDNA to mRNA, clone_1fb:PLACE1
             clone:PLACE1009493.
ORGANISM     Homo sapiens
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
             Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE    1
AUTHORS      Iisoga,T., Oca,T., Hayashi,K., Sugiyama,T., Otsuki,T., Suzuki,Y.,
             Nishikawa,T., Nagai,K., Sugano,S., Shitatori,A., Sudo,H.,
             Wagaatsuma,M., Hosoi,T., Kaku,Y., Kodaira,H., Kondo,H.,
             Sugawara,M., Takahashi,M., Chiba,Y., Ishida,S., Murakawa,K.,
             Ono,Y., Takuchi,S., Matanabe,S., Kimura,K., Murakami,K.,
             Ishii,S., Kawai,Y., Saito,K., Yamamoto,J., Wakamatsu,A.,
             Nakamura,Y., Nagahari,K., Masuno,Y., Niinomiya,K. and Iwayanagi,T.
TITLE        NEO human cDNA sequencing project
JOURNAL      Unpublished
REFERENCE    2 (bases 1 to 1813)
AUTHORS      Iisoga,T. and Otsuki,T.
TITLE        Direct Submission
JOURNAL      Submitted (23-AUG-2000) Takao Iisoga, Helix Research Institute,
             Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
             (E-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)
             NEO human cDNA sequencing project supported by Ministry of
             International Trade and Industry of Japan: cDNA full insert
             sequencing: Research Association for Biotechnology; cDNA library
             construction; 5'- & 3'-end one pass sequencing and clone selection:
             Helix Research Institute (supported by Japan Key Technology Center
             etc.) and Department of Virology, Institute of Medical Science,
             University of Tokyo.
FEATURES     source
             location/qualifiers
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             /tissue_type="Placenta"
             /clone_1fb="PLACE1"
             /note="Cloning vector: pME18SFL3"
             31..1023
             /note="unnamed protein product"
             /codon_start=1
             /protein_id="PAB14629.1"
             /db_xref="GI:10435645"
             /translation="MPRLVRYEPRREHYVVLIRNFIKISTIGICCYWLVNVALS
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             ELIYAQTLWLGIFPCPLPFIOMIMLFIMFYSKNISLMNFPSSAKASQMMFEF
             IFLFPEFSGVCTLTATITMRLKPSADCGPFLPFIHISYSWIDPLSTRGYLWV
             VMIRNIGSVHFEELITLITLITTYWQITGKRIIRLHBOITNEGDKMFLIE
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BASE COUNT   489 a      400 c      405 g      519 t
ORIGIN
Alignment Scores:
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Score:        1002.00      Matches:      190
Percent Similarity: 100.00%      Conservative: 0
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Query Match:  100.00%      Indels:      0
DB:           9      Gaps:      0
US-09-895-298A-83 (1-190) x AK023655 (1-1813)
QY      1 MetMetAsnPhgAlnProProSerLysAlaTrpAlaSerGlnMetMetThrPhe 20
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Db      451 ATGATGAAATTTCCAGCCCTCCGACGAACCCCTGGCGGCGCTCACAGATGATACATTCTTC 510
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QY      21 IllePheLeuLeuPhePheProSerPheThrGlyValLeuGlyTrhrLeuAlaIleThrIle 40
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Db 511 ANCTCTTGCTCTTTTCCCATCTTCAACCGGGGCTTTGTCACCCCTGGCCATCACCATC 570
QY 41 TTPATGLeuLysProSerAlaAspCysGlyProPheArgGlyLeuProLeuPheIleHis 60
Db 571 TGGAGATTGAAGCTTCAGCTGACGTGAGCTGCTTTTCAGAGGTCTCTCTTCATTCAC 630
QY 61 SerIleTySerTrpIleAspThrLeuSerThrArgProGlyTyrLeuTrpValAlaTrp 80
Db 631 TCCATCTACAGCTGATGACACCCCTAGTACACGGCCCTGCTACTGCGGTTGTTGG 690
QY 81 IleTyrArgAsnLeuIleGlySerValHisPhePheIleLeuThrLeuIleValLeu 100
Db 691 ATCTATCGGAACCTCATGGAAGTGTGCACCTTTTTCATCTTCACCTCATTTGCTG 750
QY 101 IleIleThrTyrLeuTyrTrpGlnIleThrGluArgGlyIleMetIleArgLeuLeu 120
Db 751 ATCATCACCCTATCTTACTGCGAGATCACAGAGGAGGAAGATTAATGATTAAGCTGCTC 810
QY 121 HisGluGlnIleIleAsnGluGlyLysAspLysMetPheLeuIleGluLysLeuIleLys 140
Db 811 CATGAGCAGATCATTAATGAGGCAAGATTAATGTTCTCTGATGAAAAATTGATCAAG 870
QY 141 LeuGlnAspMetGluLysLysAlaAsnProSerSerLeuValLeuGluArgGlyVal 160
Db 871 CTGACAGATATGAGAAAGCAAAACCCACCTCATCTGTTGGAAGAGAGAGGTG 930
QY 161 GluGlnGlnGlyPheLeuHisLeuGlyLysHisAspGlySerLeuAspLeuArgSerArg 180
Db 931 GAGCAACAAGGCTTTTTCATTGGGGAAACATGATGCGAGCTTGACTTGGCATCTAGA 990
QY 181 ArgSerValGlnGluGlyAsnProArgAla 190
Db 991 AGATCATGTTCAAGAGTATTCAGAGGCC 1020

RESULT 3

AX108538

LOCUS AX108538 1960 bp DNA Linear PAT 30-APR-2001

DEFINITION Sequence 5 from Patent WO0123417.

ACCESSION AX108538

VERSION AX108538.1 GI:13923838

KEYWORDS

SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 1960)

AUTHORS Vinals y de Bassols,C.

TITLE Human tumor-associated lak-4p related polynucleotides and

JOURNAL Patent: WO 0123417-A 5 05-APR-2001;

SMITHKLINE BEECHAM BIOLOGICALS S.A. (BE)

FEATURES

source location/Qualifiers

BASE COUNT 515 a 439 c 447 g 559 t

ORIGIN

Alignment Scores:

Pred. No.: 4,17e-102 Length: 1960
Score: 1002.00 Matches: 190
Percent Similarity: 100.00% Conservative: 0
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Query Match: 100.00% Indels: 0
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US-09-895-298A-83 (1-190) x AX108538 (1-1960)

QY 1 MetMetAsnPhgGlnProProSerLysAlaTTPATGAlaSerGlnMetMetThrPhePhe 20
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Db 805 ANCTCTTGCTCTTTTCCCATCTTCAACCGGGGCTTTGTCACCCCTGGCCATCACCATC 864
QY 41 TTPATGLeuLysProSerAlaAspCysGlyProPheArgGlyLeuProLeuPheIleHis 60
Db 865 TGGAGATTGAAGCTTCAGCTGACGTGAGCTGCTTTTCAGAGGTCTCTCTTCATTCAC 924
QY 61 SerIleTySerTrpIleAspThrLeuSerThrArgProGlyTyrLeuTrpValAlaTrp 80
Db 925 TCCATCTACAGCTGATGACACCCCTAGTACACGGCCCTGCTACTGCGGTTGTTGG 984
QY 81 IleTyrArgAsnLeuIleGlySerValHisPhePheIleLeuThrLeuIleValLeu 100
Db 985 ATCTATCGGAACCTCATGGAAGTGTGCACCTTTTTCATCTTCACCTCATTTGCTG 1044
QY 101 IleIleThrTyrLeuTyrTrpGlnIleThrGluArgGlyIleMetIleArgLeuLeu 120
Db 1045 ATCATCACCCTATCTTACTGCGAGATCACAGAGGAGGAAGATTAATGATTAAGCTGCTC 1104
QY 121 HisGluGlnIleIleAsnGluGlyLysAspLysMetPheLeuIleGluLysLeuIleLys 140
Db 1105 CATGAGCAGATCATTAATGAGGCAAGATTAATGTTCTGATGAAAAATTGATCAAG 1164
QY 141 LeuGlnAspMetGluLysLysAlaAsnProSerSerLeuValLeuGluArgGlyVal 160
Db 1165 CTGACAGATATGAGAAAGCAAAACCCACCTCATCTGTTGGAAGAGAGAGGTG 1224
QY 161 GluGlnGlnGlyPheLeuHisLeuGlyLysHisAspGlySerLeuAspLeuArgSerArg 180
Db 1225 GAGCAACAAGGCTTTTTCATTGGGGAAACATGATGCGAGCTTGACTTGGCATCTAGA 1284
QY 181 ArgSerValGlnGluGlyAsnProArgAla 190
Db 1285 AGATCATGTTCAAGAGTATTCAGAGGCC 1314

RESULT 4

AX108534

LOCUS AX108534 2407 bp DNA Linear PAT 30-APR-2001

DEFINITION Sequence 1 from Patent WO0123417.

ACCESSION AX108534

VERSION AX108534.1 GI:13923834

KEYWORDS

SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 2407)

AUTHORS Vinals y de Bassols,C.

TITLE Human tumor-associated lak-4p related polynucleotides and

JOURNAL Patent: WO 0123417-A 1 05-APR-2001;

SMITHKLINE BEECHAM BIOLOGICALS S.A. (BE)

FEATURES

source location/Qualifiers

BASE COUNT 635 a 557 c 546 g 669 t

ORIGIN

Alignment Scores:

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Score: 1002.00 Matches: 190
Percent Similarity: 100.00% Conservative: 0
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DB: 6 Gaps: 0

US-09-895-298A-83 (1-190) x AX108534 (1-2407)

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QY 21 ILepheleuPhePheProSerPheThrGlyValLeuCyStrhLeuAlaIleThrIle 40
 Db 1252 ATCTTCTGGCTTTTCCCATCCTTCACCGGGGCTTGTGCACCCCGGCATCAGCATC 1311
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 Db 1312 TGGAGATTGAAGCCTTCAGCTGACTGTGGCCCTTTTCAGAGTCTGCCCTCTTCATTCAC 1371
 QY 61 SerIleYrSerTrpIleAspThrLeuSerThrArgProGlyTyrLeuTrpValValTrp 80
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 QY 141 LeuGlnAspMetGluLysLysAlaAsnProSerSerLeuValLeuGluArgGluVal 160
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 QY 161 GluGlnGlnGlyPheLeuHisLeuGlyGluHisAspGlySerLeuAspLeuArgSerArg 180
 Db 1672 GAGCAACAAGCCTTTTGGATTGGGGGAACATGATGAGCTTGTGACCTTGCATCTAGA 1731
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 RESULT 5
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 DEFINITION Sequence 3 from Patent WO0123417.
 ACCESSION AX108536
 VERSION AX108536.1 GI:13923835
 KEYWORDS
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE
 1 (bases 1 to 2521)
 AUTHORS vinals y de Bassols,C.
 TITLE Human tumor-associated lak-4p related polynucleotides and
 polypeptides and their uses
 JOURNAL Patent: WO 0123417-A 3 05-APR-2001;
 SMITHKLINE BEECHAM BIOLOGICALS S.A. (BE)
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QY 21 ILepheleuPhePheProSerPheThrGlyValLeuCyStrhLeuAlaIleThrIle 40
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 QY 41 TTPArgLeuLysProSerAlaAspCysGlyProPheArgGlyLeuProLeuPheIleHis 60
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 QY 61 SerIleYrSerTrpIleAspThrLeuSerThrArgProGlyTyrLeuTrpValValTrp 80
 Db 1486 TCCATCTACAGCTGGATCGACACCTTAAGTACAGCGCCCTGCTACCTGTGGGTGTGG 1545
 QY 81 ILeTyrArgAsnLeuIleGlySerValHisPhePheIleLeuThrLeuIleValLeu 100
 Db 1546 ATCATCGGAACCTCATTTGGAAGTGTGCACCTTTTTCATCCCTCACCCCTCATTTGCTCA 1605
 QY 101 ILeIleThrTyrLeuTyrTrpGlnIleThrGluGlyArgLysIleMetIleArgLeuLeu 120
 Db 1606 ATCATCACCTATCTTTACTGTCAGATCAGAGGGAAGGAAATTATGATTAAGGCTCTC 1665
 QY 121 HisGluGlnIleIleAsnGluGlyLysAlaAspLysMetPheLeuIleGlyLysLeuIleLys 140
 Db 1666 CATGAGCAGATCATTAATGAGGCAAAAGATTAATGTTCTCTGATAGAAAATTGATCAAG 1725
 QY 141 LeuGlnAspMetGluLysLysAlaAsnProSerSerLeuValLeuGluArgGluVal 160
 Db 1726 CTGAGAGATATGAGAGAAGAAACCCAGCTCACTTGTCTGGAAGAGAGAGAGT 1785
 QY 161 GluGlnGlnGlyPheLeuHisLeuGlyGluHisAspGlySerLeuAspLeuArgSerArg 180
 Db 1786 GAGCAACAAGCCTTTTGGATTGGGGGAACATGATGAGCTTGTGACCTTGCATCTAGA 1845
 QY 181 ArgSerValGlnGluGlyAsnProArgAla 190
 Db 1846 AGATCACTTCAAGAGTAATCCAGGGCC 1875
 RESULT 6
 LOCUS BC027602 2760 bp mRNA linear PRI 01-MAY-2002
 DEFINITION Homo sapiens, similar to RIKEN cDNA 433243J08 gene, clone
 MGC:26648 IMAGE:4839111, mRNA, complete cds.
 ACCESSION BC027602
 VERSION BC027602.1 GI:20381190
 KEYWORDS
 SOURCE MGC.
 ORGANISM Homo sapiens.
 Homo sapiens.
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE
 1 (bases 1 to 2760)
 AUTHORS Strausberg,R.
 TITLE Direct Submission
 JOURNAL Submitted (08-APR-2002) National Institutes of Health, Mammalian
 Gene Collection (MGC), Cancer Genomics Office, National Cancer
 Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
 USA
 NIH-MGC Project URL: <http://mgc.nci.nih.gov>
 Contact: MGC help desk
 Email: cgaps-remail.nih.gov
 Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
 cDNA Library Preparation: Michael J. Brownstein (NHGRI) & Shiraki
 Toshiyuki and Piero Carninci (RIKEN)
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Institute for Systems Biology
<http://www.systemsbio.org>
 Contact: anand@systemsbiology.org
 Anup Madan, Jessica Fahey, Erin Helton, Mark Kettelman, Anuradha
 Madan, Stephanie Rodrigues, Amy Sanchez and Michelle Whiting
 Clone distribution: MGC clone distribution information can be found
 through the I.M.A.G.E. Consortium/LNL at: <http://image.lnl.gov>
 Series: IRAC Plate: 34 Row: P Column: 13
 This clone was selected for full length sequencing because it

passed the following selection criteria: Genomescan gene prediction, similarity but not identity to protein.

FEATURES

Location/Qualifiers

1..2760
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="MGC:26648 IMAGE:4839111"
/tissue_type="testis"
/clone_1ib="NH_MGC_97"
/lab_host="DH10B"
/note="vector: pBluescript"
213..2495
/codon_start=1
/product="Similar to RIKEN cDNA 4932443L08 gene"
/protein_id="AAH27602.1"
/db_xref="gi:20381191"

CDS

/translation="MSPDHVEITITQYENVSSQSPSSNQIQEYVLDSSINM
LISIDVIDSVTSKNDQKNOVLRSTSLNESQSTLHSECMGIDTPSSHEV
OGKLIASLIPMTSHDRKAIKRNQRTKEKNKIVDEKSKQTHRILOQNCIOC
LNSISRAVRSKNSLSSEILNSISLMQKTLKIGKFGTSVLSFENLMLKFNIFE
ILNFEIITPOPTVAKKNTLOFTGLEPFGVGFEDTWMYGVGFNSTHOGNSGAY
NMOLAVITIGACITTCFESLIFSAKPRNNFIPHYSGGITITLCMDPTVHEK
AVKLOKNUSTEBIRENLSELROENSKLTFNQLIRFSAYAWAVSTGVALDCAAY
YLAEVNLEFLKTHSNPQAVLLPQVSCINLAVPQIYMFRLVEREYEMPRHEVYLLI
RNIFKISITIGILCYWLVNVALSGECMETLIGDIYRLMDVFSIVNLEFEL
RRIQMOLITSLGQEDIANRVLELIYAQTLWIGIFECPLPIOMIMLEIFYSK
NISLMNPOPSKARASOMTFEILFEPFGVLCITATTIRIKPSADCGPERG
LPLFHSIYSMTDITSTRPGIYMYVIRNLIGSVHFFIITLIVLITLYITWQTEG
KIMIRLHEQITNEKDMFLTEKLIRKLODEKKNANPSLVEREVEQOQFHLHGE
HDGSLDLSRSRVQGNPRA"

BASE COUNT
ORIGIN

739 a 637 c 625 g 759 t

Alignment Scores:

Pred. No.: 6,44e-102 Length: 2760
Score: 1002.00 Matches: 190
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
Gaps: 9

US-09-895-298a-83 (1-190) x BC027602 (1-2760)

1 MetMetAspNheGlnProProSerLysAlaTrpArgAlaSerGlnMetMetTrpPhe 20
1923 ATGATGAAATTTCCAGCCTCCGACCAAGCCTGCGGCGCTCACAGATGATGATTTCTTC 1982
21 IlePheLeuLeuPhePheProSerPhePheGlyValLeuGlyThrLeuAlaIleThrIle 40
1983 ATCTCTTGCTTTTCCATCCATCCCTCACCGGGCTGTGAGCACTCGGCATCACCATC 2042
41 TrpArgLeuLysProSerAlaAspCysGlyProPheArgGlyLeuProLeuPheIleHis 60
2043 TGGAGATTGAAAGCCTTCAGCTGACTGTGGCCCTTTTCGAGGTCCTGCTCTTCATTCAC 2102
61 SerIleTyrSerTrpIleAspThrLeuSerThrArgProGlyTyrIleuTrpValValTrp 80
2103 TCCATCTACAGCTGATCGACACCTTAAGTACCGGCTGCGTACCTGAGGTTGTTGG 2162
81 IleTyrArgAsnLeuIleGlySerValHisPhePheIleLeuThrLeuIleValIleu 100
2163 ATCTATCGGAACCTCATTTGGAAGTGTGCACTCTTTTTCATCTCCACCCCATTTGGCTA 2222
101 IleIleThrTyrLeuTyrTrpGlnIleThrGluGlyArgGlyIleMetIleArgLeuLeu 120
2223 ATCATGACCATTCATTACTGCGAGATCACAGAGGAAGATTTATGATTAAGCTGCTC 2282
121 HisGluGlnIleIleAsnGluGlyAspLysMetPheLeuIleGluLysIleuIleLys 140
2283 CATGACGAGATCTTAATGAGGCGCAAGATTAATGTCTCTGATAGAAAAATTGATCAAG 2342
141 LeuGlnAspMetGluLysLysAlaAsnProSerSerLeuValLeuGluArgArgGluVal 160

Db 2343 CTGCAGGATATGAGAGAAAGCAAAACCCACCTCATTGTTCTGGAAGAGAGAGGTG 2402

Oy 161 GluGlnGlnGlyPheLeuHisLeuGlyLysHisAspGlySerLeuAspLeuArgSerArg 180

Db 2403 GAGCAACAAGCCTTTTTCGATTTGGGGGGAACATGATGAGCAGCTTTCATCTTGGGATCTTACA 2462

Oy 181 ArgSerValGlnGluGlyAsnProArgAla 190

Db 2463 AGATCAGTTCAAGAAAGTATCAACAGGCC 2492

RESULT 7

AK093944
LOCUS

DEFINITION Homo sapiens CDNA FLJ36625 fis, clone TRACH2017368, weakly similar to Homo sapiens mRNA for LAK-4p.

ACCESSION

AK093944.1 GI:21752906

KEYWORDS

oligo capping; fis (full insert sequence);
Homo sapiens trachea CDNA to mRNA, clone_1ib:TRACH2
clone:TRACH2017368.

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE

1

Suzuki, O., Sasaki, N., Aotsuka, S., Shoji, T., Ichihara, T.,
Shiohata, N., Matsumoto, R., Hirano, S., Sano, S., Nomura, R.,
Yoshioka, Y., Matsumura, Y., Moriya, S., Chiba, E., Momiyama, H.,
Onogawa, S., Kaeriyama, S., Satoh, N., Matsunaga, H., Takahashi, E.,
Katoaka, R., Kuga, N., Kuroda, A., Satoh, I., Kamata, K., Takami, S.,
Terashima, Y., Watanabe, M., Sugiyama, T., Irie, R., Otsuki, T.,
Sato, H., Ota, T., Wakamatsu, A., Ishii, S., Yamamoto, J., Isono, Y.,
Kawai-Hio, Y., Saito, K., Nishikawa, T., Kimura, K., Yamashita, H.,
Matsuo, K., Nakamura, Y., Sekine, M., Kikuchi, H., Kanda, R.,
Wagatsuma, M., Murakawa, K., Kaneshiro, K., Takahashi-Pujji, A.,
Oshima, A., Sugiyama, A., Kawakami, B., Suzuki, Y., Sugano, S.,
Nagahara, K., Masuno, Y., Nagai, K. and Isogai, T.
NEDO human cDNA sequencing project

Unpublished
2 (bases 1 to 2387)

REFERENCE

1

Isogai, T. and Yamamoto, J.
Direct Submission
Submitted (04-JUL-2002) Takao Isogai, FLJ Project (HRI Team); 2-6-7
Kazusa-Kamata, I. Saitaru, Chiba 292-0812, Japan
(E-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)
NEDO human cDNA sequencing project supported by Ministry of
Economy, Trade and Industry of Japan; CDNA full insert sequencing:
Research Association for Biotechnology (RAB); CDNA library
construction: Helix Research Institute (HRI) (supported by Japan
key Technology Center etc.); 5'- & 3'-end one pass sequencing: RAB,
HRI, and Biotechnology Center, National Institute of Technology and
Evaluation; clone selection for full insert sequencing: HRI and
RAB; annotation: HRI and RAB.

FEATURES

Location/Qualifiers

1..2387

/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="TRACH2017368"
/tissue_type="trachea"
/clone_1ib="TRACH2"
/note="cloning vector: pME18SFL3"

BASE COUNT
ORIGIN

624 a 549 c 543 g 671 t

Alignment Scores:

Pred. No.: 3.24e-101 Length: 2387
Score: 995.00 Matches: 189
Percent Similarity: 99.47% Conservative: 0
Best Local Similarity: 99.47% Mismatches: 1
Query Match: 99.30% Indels: 0
Gaps: 9

US-09-895-298a-83 (1-190) x AK093944 (1-2387)

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QY      1 MetetAsnphcInPrOpSerLySaLaTrPaRgAlaSerGlnMetetRhphe 20
      1025 ATGATGAATTTCCAGCTCCGAGCAAGCCTGGCGGCTCGCAGATGATGACTTTCTTC
QY      21 IlePheLeuLeuPhePheProSerPheThGlyValLeuysThrLeuAlaIleThrIle 40
      1085 ATCTCTTGCTCTTTTCCATCCCTTCACCGGGGTCTTGACACCCCGGCATCACCATC
QY      41 TrpArgLeuysProSerAlaAspCySgLyPrOpPheArgLyLeuProLeuPheIleHis 60
      1145 TGGAGATTGAAGCCTTAGCTGACTGTGGCCCTTTTCGAGTCTGCCTCTTCATTAC 1204
QY      61 SerIleTySerTrpIleAspThrLeuSerThrArgProGlyTyTrLeuTrpValValTrp 80
      1205 TCCATCTACAGCTGATGACACCCCTTAAGTACACGGCCTGGCTACGTGGGTGTGG 1264
QY      81 IleTyArgAsnLeuIleGlySerValHisPhePheIleLeuThrLeuIleValLeu 100
      1265 ATCATCGGAACCTCATTTGAAAGTGTGACTCTTTTTCATCCCTCACCCCTCATTTGCTA 1324
QY      101 IleIleThrTyLeuTyTrpGlnIleThrGlyValArgLySileMetIleArgLeuLeu 120
      1325 ATCATCCACCATCTTTCTGTCGACATCACAGAGGAAAGATATGATTAAGCTCTCTC 1384
QY      121 HisGlyGlnIleIleAsnGlyLyAspLySMeThrPheLeuIleGlyLySleuIleLys 140
      1385 CATGAGCAGATTCATTAATGAGGCAAGATAAATGTTCTCGATAGGAAATGATCAAG 1444
QY      141 LeuGlnAspMetGlyLySlySaLaAsnProSerSerLeuValLeuGlnValArgGlnVal 160
      1445 CTGAGGATATGAGAAAGAAAGCAACCCAGCTCACTTTCTTGGAAGAGAGAGCTG 1504
QY      161 GluGlnGlnIlePheLeuHisLeuGlyGlyHisAspGlySerLeuAspLeuArgSerArg 180
      1505 GAGCAACAAGCCTTTTGCATTTGGGGGAACATGATGCGAGTCTTGATCGCATCTAGA 1564
QY      181 ArgSerValGlnGlyLyAsnProArgAla 190
      1565 AGATCACTTCAGAGAGTATCCAGAGGCC 1594
Db      1565 AGATCACTTCAGAGAGTATCCAGAGGCC 1594

RESULT 8
LOCUS      AK097718      2399 bp      mRNA      linear      PRI 15-JUL-2002
DEFINITION Homo sapiens cDNA FLJ40399 fis, clone TEST12037081, weakly similar
              to Homo sapiens mRNA for LAR-4p.
ACCESSION  AK097718
VERSION     AK097718.1 GI:21757573
KEYWORDS   oligo capping, fis (full insert sequence).
SOURCE      Homo sapiens testis cDNA to mRNA, clone_lib:TEST12
              clone:TEST12037081.
ORGANISM    Homo sapiens
              Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
AUTHORS     Oshima,A., Takahashi,Fujii,A., Tanase,T., Imose,N., Takeuchi,K.,
              Arita,M., Mutsashino,K., Yuuki,H., Hara,H., Sugiyama,T., Irie,R.,
              Otsuki,T., Sato,H., Wakamatsu,A., Ishii,S., Yamamoto,T., Isono,Y.,
              Kawai-Hio,Y., Saito,K., Nishikawa,T., Kimura,K., Yamashita,H.,
              Matsuo,K., Nakamura,Y., Sekine,M., Kikuchi,H., Kanda,K.,
              WagaTsuna,M., Murakawa,K., Kanehori,K., Sugiyama,A., Kawakami,B.,
              Suzuki,Y., Sugano,S., Nagahari,K., Masuhio,Y., Nagai,K. and
              Isogai,T.
TITLE       NED0 human cDNA sequencing project
JOURNAL     Unpublished
              2 (bases 1 to 2399)
              Isogai,T. and Yamamoto,T.
              Direct Submission
              Submitted (04-JUL-2002) Takao Isogai, FLJ Project(HRI Team); 2-6-7
              Kazusa-Kametari, Kisarazu, Chiba 292-0812, Japan
              (E-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)
              NED0 human cDNA sequencing project supported by Ministry of
              Economy, Trade and Industry of Japan; cDNA full insert sequencing:
              Research Association for Biotechnology (RAB); cDNA library

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construction: Helix Research Institute (HRI) (supported by Japan
key Technology Center etc.); 5'- and 3'-end one pass sequencing: RAB,
HRI, and Biotechnology Center, National Institute of Technology and
Evaluation; clone selection for full insert sequencing: HRI and
RAB; annotation: HRI and RAB.
FEATURES             Location/Qualifiers
     source            1..2399
                        /organism="Homo sapiens"
                        /db_xref="taxon:9606"
                        /clone="TEST12037081"
                        /tissue_type="testis"
                        /clone_lib="TEST12"
                        /note="cloning vector: pME18SFL3"
BASE COUNT           610 a      591 c      528 g      670 t
ORIGIN
Alignment Scores:
Pred. No.:           5,14e-66      Length:      2399
Score:               680.00      Matches:      126
Percent Similarity:  100.00%      Conservative: 0
Best Local Similarity: 100.00%      Mismatches:  0
Query Match:         67.86%      Indels:       0
DB:                  9      Gaps:         0

US-09-895-298a-83 (1-190) x AK097718 (1-2399)
QY      1 MetetAsnphcInPrOpSerLySaLaTrPaRgAlaSerGlnMetetRhphe 20
      1025 ATGATGAATTTCCAGCTCCGAGCAAGCCTGGCGGCTCGCAGATGATGACTTTCTTC
QY      21 IlePheLeuLeuPhePheProSerPheThGlyValLeuysThrLeuAlaIleThrIle 40
      1993 ATCTCTTGCTCTTTTCCATCCCTTCACCGGGGTCTTGACACCCCTGCATCACCATC 2052
QY      41 TrpArgLeuysProSerAlaAspCySgLyPrOpPheArgLyLeuProLeuPheIleHis 60
      2053 TGGAGATTGAAGCCTTAGCTGACTGTGGCCCTTTTCGAGTCTGCCTCTTCATTAC 2112
QY      61 SerIleTySerTrpIleAspThrLeuSerThrArgProGlyTyTrLeuTrpValValTrp 80
      2113 TCCATCTACAGCTGAGATGAGACACCCCTTAAGTACACGGCCTGGCTGCTGTGGTGTGG 2172
QY      81 IleTyArgAsnLeuIleGlySerValHisPhePheIleLeuThrLeuIleValLeu 100
      2173 ATCATCGGAACCTCATTTGAAAGTGTGACTCTTTTTCATCCCTCACCCCTCATTTGCTA 2232
QY      101 IleIleThrTyLeuTyTrpGlnIleThrGlyValArgLySileMetIleArgLeuLeu 120
      2233 ATCATCCACCATCTTTCTGTCGACATCACAGAGGAAAGATATGATTAAGCTCTCTC 2292
QY      121 HisGlyGlnIleIleAsn 126
      2293 CATGAGCAGATCATTAAT 2310
Db      2293 CATGAGCAGATCATTAAT 2310

RESULT 9
LOCUS      HU091321      220633 bp      DNA      linear      PRI 10-JAN-2000
DEFINITION Human Chromosome 16 BAC clone CIT987SK-A-363B6, complete sequence.
ACCESSION  U91321
VERSION     U91321.1 GI:2951946
KEYWORDS   HTG.
SOURCE      Homo sapiens
              Homo sapiens
              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 220633)
AUTHORS     Loftus,B.J., Kim,U.J., Sneddon,V.P., Kalush,F., Brandon,R.,
              Fuhrmann,J., Mason,T., Crosby,M.L., Barnstead,M., Cronin,L.,
              Deslattes Mays,A., Cao,Y., Xu,R.X., Kang,H.L., Mitchell,S.,
              Eichler,E.F., Harris,P.C., Venter,J.C. and Adams,M.D.
TITLE       Genome duplications and other features in 12 Mb of DNA sequence
              from human chromosome 16p and 16q
              Genomics 60 (3), 295-308 (1999)
JOURNAL

```



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MEDLINE      99425270
PUBMED      10493829
REFERENCE    2 (bases 1 to 220633)
AUTHORS      Adams,M.D., Loftus,B.J., Phillips,C.A., Zhou,L., Brandon,R.,
              Fuhrmann,J. and Venter,J.C.
TITLE        Direct Submission
JOURNAL      Submitted (04-MAR-1997) The Institute for Genomic Research, 9712
              Medical Center Dr., Rockville, MD 20850, USA
REFERENCE    3 (bases 1 to 220633)
AUTHORS      Adams,M.D., Loftus,B.J., Zhou,L. and Labombard,M.
TITLE        Direct Submission
JOURNAL      Submitted (21-MAY-1997)
              Adams,M.D., Loftus,B.J., Zhou,L., La Bombard,M., Kim,U.J. and
              Venter,J.C.
REFERENCE    4 (bases 1 to 220633)
AUTHORS      Adams,M.D., Loftus,B.J., Zhou,L., La Bombard,M., Kim,U.J. and
              Venter,J.C.
TITLE        Direct Submission
JOURNAL      Submitted (19-AUG-1997) The Institute for Genomic Research, 9712
              Medical Center Dr., Rockville, MD 20850, USA
REFERENCE    5 (bases 1 to 220633)
AUTHORS      Adams,M.D., Loftus,B.J., Zhou,L., La Bombard,M., Kim,U.J. and
              Venter,J.C.
TITLE        Direct Submission
JOURNAL      Submitted (22-AUG-1997) The Institute for Genomic Research, 9712
              Medical Center Dr., Rockville, MD 20850, USA
REFERENCE    6 (bases 1 to 220633)
AUTHORS      Adams,M.D.
TITLE        Direct Submission
JOURNAL      Submitted (11-MAR-1998) The Institute for Genomic Research, 9712
              Medical Center Dr., Rockville, MD 20850, USA
COMMENT      On Mar 11, 1998 this sequence version replaced gi:2335062.
              BAC clone C198787K-363E6 is located in band 16p13.1 of chromosome
              16. Genes were identified by a combination of five methods:
              XGAPIL (available by anonymous ftp from arthur.epm.ornl.gov),
              GeneFinder (available by anonymous ftp from
              colinle.washington.edu), GENSCAN (available using the e-mail server
              at genescan@omic.stanford.edu), searches of the EST database at
              TIGR (http://www.tigr.org/tdb/hcd/hcd.html) and searches against a
              peptide database. Repeats were identified using RepeatMasker (Smrt,
              A.F.A. and Green, P. unpublished,
              http://ftp.genome.washington.edu/rm/RepeatMasker.html).
FEATURES
SOURCE
LOCATION/Qualifiers
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="16"
/map="16p13.1"
/clone="A-363E6"
/complement(82033..108338)
/gene="363E6.1"
/complement(join(82033..82152,82283..82349,107848..108338))
/gene="363E6.1"
/complement(join(82117..82152,82283..82349,107848..107915))
CDS
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/codon_start=1
/product="Unknown gene product"
/db_xref="GI:2951947"
/translation="WPTRPQPPVPRFLTSSQERLHRCWTRRLSPDAGLVILDFPAPR
TIMAPSAWFILE"
/gene="363E6.2"
/complement(join(217478..219568))
/gene="363E6.2"
/complement(join(217478..218093,219357..219568))
/gene="363E6.2"
/complement(join(217946..218093,219357..219568))
CDS
/gene="363E6.2"
/codon_start=1
/product="Unknown gene product"
/db_xref="GI:2951948"
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/translation="WRQTRDQVITLALTRPWSLSHTGDKPRYDTFMKHFIFVMDIL
LDWSMHNILWYLCGISAFILMOKDFVSPAYLAKWSAKGIQVVGWTVNTDEKSYESH
GSSYITDMSVECEBPH"
BASE COUNT  61048 a 48977 c 49108 g 61449 t 51 others

```

```

ORIGIN
Alignment Scores:
Pred. No.: 4.39e-24
Score: 327.00
Percent Similarity: 96.83%
Best Local Similarity: 95.24%
Query Match: 32.63%
DB: 9 Gaps: 0
US-09-895-298a-83 (1-190) x HU091321 (1-220633)
QY 42 ATGLeuLysPProSerAlaaspCysGlyProPheArgGlyLeuProLeuPheIleHisSer 61
|||||
DB 204866 AGATTGAAGCCTTCACGCTGACGTGGCCCTTTTCAGAGCTGCTCTTCATTACATCC 204925
|||||
QY 62 ILeYrSerTrpIleAspThrLeuSerThrArgProGlyTrpValValTrpIle 81
|||||
DB 204926 ATCTACAGCTGGATGACACCCCTTAAGTACACGCGCTGGCTACTGTGGTTGTTGATC 204985
|||||
QY 82 TYrArgAsnLeuIleGlySerValHisPhePheIleLeuThrLeuValLeuIle 101
|||||
DB 204986 TATCGAACCCTGATTGGAAGTGTGACCTTTTCATCCTCACCCCATTTGTGCTGGA 205045
|||||
QY 102 ILeThrTrp 104
::: |||
DB 205046 GTGTGCTAC 205054
RESULT 10
AC130456 223280 bp DNA linear HTG 10-AUG-2002
AC130456
LOCUS
DEFINITION Homo sapiens chromosome 16 clone CTA-363E6, WORKING DRAFT SEQUENCE,
5 unordered pieces.
ACCESSION AC130456
VERSION AC130456.1 GI:22203229
KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ACTIVEFTN.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 223280)
DOE Joint Genome Institute.
Sequencing of Human Chromosome 16
Unpublished
2 (bases 1 to 223280)
DOE Joint Genome Institute.
Direct Submission
Submitted (10-AUG-2002) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
-----Genome Center
Center: Joint Genome Institute
Center Code: JGI
Web site: http://www.jgi.doe.gov
-----
Project Information
Center Project Name: C1978SKA_363E6
Center clone name: C1978SKA_363E6
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Summary Statistics
Consensus quality: 221100 bases at least Q40
Consensus quality: 222027 bases at least Q30
Consensus quality: 222494 bases at least Q20
Estimated insert size: 220633; agarose-1p estimation
Estimated insert size: 222880; sum-of-ctnigs estimation
Quality coverage: 10.71 in Q20 bases; agarose-1p estimation
Quality coverage: 10.71 in Q20 bases; sum-of-ctnigs estimation.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 5 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will

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* be preserved.
* 1 1261: contig of 1261 bp in length
* 1262 1361: gap of unknown length
* 12690: contig of 1329 bp in length
* 2691 2790: gap of unknown length
* 2791 32134: contig of 29344 bp in length
* 32135 32234: gap of unknown length
* 32235 102578: contig of 70344 bp in length
* 102579 102679: gap of unknown length
* 223280: contig of 120602 bp in length.
FEATURES
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        /db_xref="taxon:9606"
        /chromosome="16"
        /clone.lib="Caltech human BAC library A"
        /clone.lib="Caltech human BAC library A"
BASE COUNT  61286 a 49953 c 49351 g 62289 t 401 others
ORIGIN
Alignment Scores:
Pred. No.:      4..46e-24      Length:      223280
Score:          327.00         Matches:      60
Percent Similarity: 96.83%      Conservative: 1
Best Local Similarity: 95.24%      Mismatches:  2
Query Match:     32.63%         Indels:      0
DB:              2             Gaps:         0

US-09-895-298a-83 (1-190) x AC130456 (1-223280)
QY  42 ArgLeuLysProSerAlaIspCysGlyProPheArgGlyLeuProLeuPheIleHisSer 61
    |||||||
Db  86822 AGATTGAAGCCTTCAGCTGACTGTGGCCCTTTTCGAGAGCTGCTCCTCATTCACCTCC 86881
QY  62 ILeTySerTrpIleAspTrpTrpLeuSerThrArgProGlyTyLeuTrpValValTrpIle 81
    |||||||
Db  86882 ATCTACAGCTGGATCGACACCTCAGACGGCTGGCTGCTACCTGGTGGTTGGATTC 86941
QY  82 TyrArgAsnLeuIleGlySerValHisPhePheIleLeuThrLeuIleValIleuile 101
    |||||||
Db  86942 TATCGGAACCTCAATGGAATGTGCACCTTCTTTTCTCCTCACCCCATTCGTCGTGA 87001
QY  102 ILeThrTyr 104
    ::: |||
Db  87002 GTGTGTGTAC 87010

RESULT 11
AC100877 71596 bp DNA linear HTG 23-NOV-2001
LOCUS      Mus musculus clone RP23-35B17, LOW-PASS SEQUENCE SAMPLING.
AC100877
AC100877.1 GI:17059651
VERSION    HTG: HTGS PHASE0.
KEYWORDS   Mus musculus.
SOURCE     Mus musculus.
ORGANISM   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE  1 (bases 1 to 71596)
AUTHORS    Birren, B., Linton, L., Nusbaum, C. and Lander, E.
TITLE      Unpublished
JOURNAL    2 (bases 1 to 71596)
REFERENCE  2 (bases 1 to 71596)
AUTHORS    Birren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N.,
            Anderson, S., Barin, N., Bastien, V., Boguslavsky, L., Boukhalter, B.,
            Brown, A., Camarata, J., Campopiano, A., Chang, J., Chazaro, B.,
            Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cook, A.,
            Coote, P., Dearellano, K., Dewar, K., Diaz, J. S., Dodge, S., Faro, S.,
            Ferreira, P., Fitzhugh, W., Gage, D., Galagan, J., Gardyna, S.,
            Ginde, S., Gord, S., Goyette, M., Graham, L., Grand-Pierre, N.,
            Hages, B., Headford, A., Horton, L., Hulme, W., Iliev, I., Johnson, R.,
            Jones, C., Kamat, A., Karatas, A., Kells, C., LaRoque, K.,
            Lamazares, R., Landers, T., Lehoczy, J., Levine, R., Liu, G.,
            Maclean, C., Macdonald, P., Major, J., Margulis, N., Matthews, C.,

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TITLE
JOURNAL
COMMENT
McCarthy, M., McEwan, P., McKernan, K., McPheeters, R., Meldrum, J.,
Meneus, L., Minova, T., Mlenga, V., Murphy, T., Naylor, J., Nguyen, C.,
Norbu, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neill, D.,
Olivier, J., Peterson, K., Phunkhang, P., Pierre, N., Pollara, V.,
Raymond, C., Retta, R., Rieback, M., Riley, R., Riese, C., Rogov, P.,
Roman, J., Rosetti, M., Roy, A., Santos, R., Schauer, S., Schnpbach, R.,
Seaman, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N.,
Strauss, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J.,
Topham, K., Travers, M., Travis, N., Triggillo, J., Vassiliev, H.,
Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G.,
Zainou, J., Zembek, L., Zimmer, A. and Zody, M.
Direct Submission
Submitted (23-NOV-2001) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
----- Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIBR
Web site: http://www-seq.wi.mit.edu
Contact: sequence.submissions@genome.wi.mit.edu
----- Project Information
Center project name: L13918
Center clone name: 35_B_17
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* NOTE: This record contains 87 individual
* sequencing reads that have not been assembled into
* contigs. Runs of N are used to separate the reads
* and the order in which they appear is completely
* arbitrary. Low-pass sequence sampling is useful for
* identifying clones that may be gene-rich and allows
* overlap relationships among clones to be deduced.
* However, it should not be assumed that this clone
* will be sequenced to completion. In the event that
* the record is updated, the accession number will
* be preserved.
1
* 723 822: contig of 722 bp in length
* 823 1526: contig of 704 bp in length
* 1527 1626: gap of 100 bp
* 1627 2336: contig of 710 bp in length
* 2337 2436: gap of 100 bp
* 2437 3156: contig of 720 bp in length
* 3157 3256: gap of 100 bp
* 3257 3984: contig of 728 bp in length
* 3985 4084: gap of 100 bp
* 4085 4811: contig of 727 bp in length
* 4812 4911: gap of 100 bp
* 4912 5638: contig of 727 bp in length
* 5639 5738: gap of 100 bp
* 5739 6477: contig of 739 bp in length
* 6478 6577: gap of 100 bp
* 6578 7305: contig of 728 bp in length
* 7306 7405: gap of 100 bp
* 7406 8107: contig of 702 bp in length
* 8108 8207: gap of 100 bp
* 8208 8950: contig of 743 bp in length
* 8951 9050: gap of 100 bp
* 9051 9743: contig of 693 bp in length
* 9744 9843: gap of 100 bp
* 9844 10583: contig of 740 bp in length
* 10584 10683: gap of 100 bp
* 10684 11405: contig of 722 bp in length
* 11406 11505: gap of 100 bp
* 11506 12236: contig of 731 bp in length
* 12237 12336: gap of 100 bp
* 12337 13069: contig of 733 bp in length
* 13070 13169: gap of 100 bp
* 13170 13851: contig of 682 bp in length
* 13852 13951: gap of 100 bp
* 13952 14685: contig of 734 bp in length
* 14686 14785: gap of 100 bp

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ALIGNMENT SCORES:	PROTEIN NO.:	SCORE:	PERCENT SIMILARITY:	BEST LOCAL SIMILARITY:	QUERY MATCH:	DB:
45139	45238	gap of	100 bp			
45239	45976	contig of 738 bp	in length			
45977	46076	gap of	100 bp			
46077	46808	contig of 732 bp	in length			
46809	46908	gap of	100 bp			
46909	47613	contig of 705 bp	in length			
47614	47713	gap of	100 bp			
47714	48431	contig of 718 bp	in length			
48432	48531	gap of	100 bp			
49281	49380	gap of	100 bp			
49381	50139	contig of 759 bp	in length			
50140	50238	gap of	100 bp			
50240	50966	contig of 727 bp	in length			
50967	51066	gap of	100 bp			
51067	51797	contig of 731 bp	in length			
51798	51897	gap of	100 bp			
51898	52632	contig of 735 bp	in length			
52633	52732	gap of	100 bp			
52733	53448	contig of 716 bp	in length			
53449	53548	gap of	100 bp			
53549	54266	contig of 718 bp	in length			
54267	54366	gap of	100 bp			
54367	55107	contig of 741 bp	in length			
55108	55207	gap of	100 bp			
55208	55927	contig of 720 bp	in length			
55928	56027	gap of	100 bp			
56028	56757	contig of 730 bp	in length			
56758	56857	gap of	100 bp			

ALIGNMENT SCORES:	PROTEIN NO.:	SCORE:	PERCENT SIMILARITY:	BEST LOCAL SIMILARITY:	QUERY MATCH:	DB:
1.81e-22	307.00	Matches:	71596			
92.42%	84.85%	Conservative:	5			
30.64%		Mismatches:	5			
		Indels:	0			
		Gaps:	0			

US-09-895-298A-83 (1-190) x AC100877 (1-71596)
40 IleHrPargLeuLysProSerAlaAspGlyGlyProPheArgGlyLeuProLeuPheLeu 59
Db 48651 GTCTTCACAGCAAAACCTTGCGCTGACGTGACCCCGTCCGAGGCTCCTTCCTTCATC 48710
60 HisSerIleYrSerTrpIleAspThrLeuSerThrArGProGlyTyrLeuTrpValVal 79
Db 48711 CAATCCACATCTACAGTGTGACACTGTGACGCCGACGCTGCTACTGTGGTGGTC 48770
80 TrpIleYrArGAsnLeuIleGlySerValHisPhePhePheLeuLeuThrLeuIleVal 99
Db 48771 TGGATCTTCACAGAAATTCATGTGAAGTGTGACATCTCTTCATCATCCTCACCTCATTTGTG 48830
100 LeuIleIleThrIleThrLeu 105
Db 48831 CTGTAAGTGGGGGCTTCCTC 48848

RESULT 12	LOCUS	DEFINITION	VERSION	KEYWORDS	SOURCE	ORGANISM	REFERENCE	AUTHORS	TITLE
AB002405	AB002405	Homo sapiens mRNA for LAK-4p, complete cds.	AB002405.2	GI:7209573	LAK-4p.	Homo sapiens male lymphoid.mlt expressing LAK cell cDNA to mRNA.	1639 bp	linear	PRI 02-MAR-2000
JOURNAL	REFERENCE	2 (bases 1 to 1639)				Published Only in Database (1998)			

AUTHORS Abe, Y. and Takeoka, Y.
 TITLE Direct Submission
 JOURNAL Submitted (28-MAR-1997) Yasuhito Abe, Ehime University School of Medicine, The Second Department of Surgery, Shigenobu, Onsen-gun, Ehime 791-02, Japan (E-mail: yasuhito@ehime-u.ac.jp, Tel: +81-89-964-5111, Fax: +81-89-960-5334)
 COMMENT On Mar 8, 2000 this sequence version replaced g1:2760120. Sequence updated (05-Jan-1998)
 FEATURES
 source
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 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /sex="male"
 /cell_type="mLr expressing LAK cell"
 /tissue_type="lymphoid"
 53.1387
 /note="its enhancement of expression is related with T/LAK-cell activation, unpublished data."
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 EAAGQAVLVLPVGVGLNLGAPYLCRVLALEPHDSVLEVYVAICRNLIKLA
 GLCYHMLGRVGVLOGQWEDFVGOELRYLMDVLMLEDTLEFELVWRITSEKIL
 KRRKRPEDIANRVLETIGOTLWGLVSPFLPAVOIKLLIVFYVKKSTLANCO
 APRRWLASHSMTVLTLLCPAFGLAAVFLCYAVWQKPSSTCGPFRDMDYAGR
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 1614
 polyA_site
 294 a 495 c 517 g 333 t
 BASE COUNT
 ORIGIN
 Alignment Scores:
 Pred. No.: 5.55e-23 Length: 1639
 Score: 293.00 Matches: 63
 Percent Similarity: 53.76% Conservative: 37
 Best Local Similarity: 33.87% Mismatches: 66
 Query Match: 29.24% Gaps: 20
 DB: 9
 US-09-895-298a-83 (1-190) x AB002405 (1-1639)
 QY 1 MetMetAspNheGlnProSerLysAlaTrpArgAlaSerGlnMetThrPhe 20
 Db 866 CTGGCCAACTGCCAGCGCGCGCCCTGCGCTCACACATGACACCGCTTC 925
 QY 21 IlePheLeuLeuPhePheProSerPheThyGlyValLeuGlyThrLeuAlaIle 40
 Db 926 CTCACGCTGCTGCTCCCGCGCTCCGCGCGCTGCTTCCTGCTACGCGCTG 985
 QY 41 TrpAlaGluPheProSerAlaAspGlyLysPheArgGlyLeuProLeuPheIle 60
 Db 986 TGGAGGTGAGAGCCCTGAGCACCCTGCGCCCTCGGACCTGGACACCATGACG 1045
 QY 61 SerIleTyrSerTrpIleAspThrLeu---SerThrArgProGlyTyrLeuTrpVal 79
 Db 1046 GCGGCGAGGGTGTGGTGGCCGACCTGAGAGCGCCGACGAGGCTCTGCTGCC 1105
 QY 80 TrpIleTyrArgAsnLeuIleGlySerValHisPhePheIleLeuThrLeuIle 99
 Db 1106 TGGGTGACCGGTACCGATGAGAAACACCTTCTTCTGCTGAGTACCGCTG 1165
 QY 100 LeuIleIleThrTyrLeuTyrTrpGlnIleThyGluGlyArgGlyIleMetIle 119
 Db 1166 CTGGCGGTATCTACCTCAACATCCAGGTGTCGGGGCCAGGCAAGTCATCTG 1225
 QY 120 LeuHisGluGlnIleIleAsnGluGlyLysAspLysMetPheLeuIleGlyLys 139
 Db 1226 CTCAGAGAGCATGACGATGAGGAGGAGGACAAATCTTCTTAATCAACAAGCTT 1285

QY 140 LysLeuGlnAsp-----NetGluLys 147
 Db 1286 TCCATCTACACGAGGAGAGGAGGAGGAGGCTTGGACACACCGAGGAGGCT 1345
 QY 148 AlaAspProSerLeuValLeuGluArgGlyValGluGlnGlnGlyPheLeuHis 167
 Db 1346 GCGGACACCCCTCCCTGCTCACAGATGACAGAGATGCC----- 1384
 QY 168 LeuGluGluHisAspGly 173
 Db 1385 TAGGGGACGCGCATGGG 1402
 RESULT 13
 BC018346
 LOCUS
 DEFINITION
 Homo sapiens, expressed in activated T/LAK lymphocytes, clone
 MG:8770 IMAGE:3862414, mRNA, complete cds.
 ACCESSION
 BC018346
 VERSION
 BC018346.1 GI:17390809
 KEYWORDS
 MGC.
 SOURCE
 Homo sapiens.
 ORGANISM
 Homo sapiens.
 Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 1 (bases 1 to 1804)
 Strausberg, R.
 Direct Submission
 Submitted (03-DEC-2001) National Institutes of Health, Mammalian
 Gene Collection (MGC), Cancer Genomics Office, National Cancer
 Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
 USA
 NIH-MGC Project URL: http://mgc.ncl.nih.gov
 Contact: MGC help desk
 Email: cgaabs-remail.nih.gov
 Tissue Procurement: DCTP/DRP
 CDNA Library Preparation: Life Technologies, Inc.
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
 DNA Sequencing by: Baylor College of Medicine Human Genome
 Sequencing Center
 Center code: BCM-HGSC
 Web site: http://www.hgsc.bcm.tmc.edu/cdna/
 Contact: villalona@bcm.tmc.edu.
 Villalón, D.K., Luna, R.A., Hale, S.M., Huilyk, S., Lu, X., García,
 A.M., Holloway, M., Telford, B., Hodgson, A., Bouck, J., Yu, W.,
 Muzny, D.M., Gibbs, R.A.

REMARK

Clone distribution: MGC clone distribution information can be found
 through the I.M.A.G.E. Consortium/LINL at: http://image.llnl.gov
 Series: IRAC Plate: 21 Row: 9 Column: 17
 This clone was selected for full length sequencing because it
 passed the following selection criteria: matched mRNA g1: 7305226.
 Location/Qualifiers
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 /db_xref="locusID:11322"
 /db_xref="taxon:9606"
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 /tissue_type="Ovary, adenocarcinoma"
 /clone_lib="NH.MGC_66"
 /lab_host="pH10B"
 /note="Vector: PCMV-SPORT6"
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 /codon_start=1
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 /protein_id="BAH18346.1"
 /db_xref="GI:17390810"

FEATURES

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 /organism="Homo sapiens"
 /db_xref="locusID:11322"
 /db_xref="taxon:9606"
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 /clone_lib="NH.MGC_66"
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 /protein_id="BAH18346.1"
 /db_xref="GI:17390810"

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 GLCYHMLGRVGVLOGQWEDFVGOELRYLMDVLMLEDTLEFELVWRITSEKIL
 KRRKRPEDIANRVLETIGOTLWGLVSPFLPAVOIKLLIVFYVKKSTLANCO
 APRRWLASHSMTVLTLLCPAFGLAAVFLCYAVWQKPSSTCGPFRDMDYAGR
 VVYRHLAAGPRVSWLPWVRYLMENTFFVLVSALLAVIYINQVVGQKRYICLL
 KEQISNEGDKITLTKLHSTYERKERERSRVGTTEAAPALTLDDQA"

KEQJISNGBEDKIFLNLKLSIYERKERERERSVGTTEBAAPALITDEQDA"

BASE COUNT 333 a 555 c 558 g 358 t

ORIGIN

Alignment Scores:

Pred. No.:	Length:	Matches:	Conservative:	Mismatches:	Indels:	Gaps:
6.27e-23	1804	63	37	66	20	
Score:	293.00					
Percent Similarity:	53.76%					
Best Local Similarity:	33.87%					
Query Match:	29.24%					

US-09-895-298a-83 (1-190) x BC018346 (1-1804)

QY 1 MetMetasnpheglProProserlysAlaTPrArgAlaSerGlnMetMetThrPhePhe 20

DB 1022 CTGGCCAACTGCCAGCGCCGCCGCGCTGGCTCTACACATGACGACCGCTTCG 1081

QY 21 IlePheLeuLeuPhePheProSerPheThrGlyValLeuCyThrLeuAlaIleThrIle 40

DB 1082 CTCACGCTGCTGCTGCTCCCGCTTCCTGGCGCGCGCTGCTTCCTGCTACCGCGTC 1141

QY 41 TrpArgLeuLysProSerAlaAspCysGlyProPheArgGlyLeuProLeuPheIleHis 60

DB 1142 TGGCAGGTGAAGCCCTCGACACCTGCGGCCCTTCGACCCCTGACACATGTACGAG 1201

QY 61 SerIleTyrSerTrpIleAspThrLeu---SerThrArgProGlyTyrIleuTrpAlaVal 79

DB 1202 GCCGGCAGGCTGGTGGTGGCGCCTGAGGCGGCGGCGGCGCTCTCGTGGCTGCC 1261

QY 80 TrpIleTyrArgAsnLeuIleGlySerValHisPhePheIleuThrIleuLeuVal 99

DB 1262 TGGGTGACACCGCTACTGATGGAANAACCTCTTGTCTTCTGCTGTCACCGCTCG 1321

QY 100 LeuIleIleThrTyrLeuTyrTrpIleIleThrGlyArgLysIleMetIleArgLeu 119

DB 1322 CTGGCGGTGATCTACCTCAACATCCAGGTGCGCGGCGGCGGCGGCGGCTGCTG 1381

QY 120 LeuHisGlnGlnIleIleAsnGlnGlyLysAspLysMetPheLeuIleGlyLysLeuIle 139

DB 1382 CTCAGGACACATGATGACATGAGGTGAGACAAATCTCTTAATCAACAAGCTTCAC 1441

QY 140 LysLeuGlnAsp-----MetGlnLysLys 147

DB 1442 TCCATCTACGAGAGAGAGAGAGAGAGAGAGAGGCTTGGGCAACCGAGGAGCT 1501

QY 148 AlaAsnProSerSerLeuValLeuGluArgGluValGlnGlnGlnIlePheLeuHis 167

DB 1502 GCGGACACCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1540

QY 168 LeuGlyGlnHisAspGly 173

DB 1541 TAGGGGAGCGGCGATGGG 1558

RESULT 14

AK074065

LOCUS AK074065 5291 bp mRNA linear PRI 15-FEB-2002

DEFINITION Homo sapiens mRNA for FLJ00136 protein.

ACCESSION AK074065

VERSION AK074065.1 GI:18676477

KEYWORDS fls (full insert sequence).

SOURCE Homo sapiens adult spleen cDNA to mRNA, clone: FLJ00136.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE 1 Jikuya,H., Takano,J., Nomura,N., Kikuno,R., Nagase,T. and Ohara,O. Title The nucleotide sequence of a long cDNA clone isolated from human spleen

JOURNAL Published Only in Database (2002)

REFFERENCE 2 (bases 1 to 5291)

AUTHORS Jikuya,H., Takano,J., Nomura,N., Kikuno,R., Nagase,T. and Ohara,O.

TITLE Direct Submission

JOURNAL

Submitted (21-Jan-2002) Takahiro Nagase, Kazusa DNA Research Institute, Department of Human Gene Research; 1532-3, Yana, Kisarazu, Chiba 292-0812, Japan (E-mail:cdna@kazusa.or.jp, URL: http://www.kazusa.or.jp/NEDO, Tel: 81-438-52-3913, Fax: 81-438-52-3914)

COMMENT

NEDO human cDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan; cDNA full insert and 5'- 3'-end one pass sequencing; Research Association for Biotechnology; cDNA library construction and clone selection; Kazusa DNA Research Institute.

FEATURES

source

1. 5291

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="FLJ00136"

/tissue="spleen"

/dev_stage="adult"

/note="vector:pBluescriptII SK plus"

1. 5291

/gene="FLJ00136"

<143. 2578

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/note="Start codon is not identified."

/codon_start=1

/evidence="not_experimental"

/product="FLJ00136 protein"

/protein_id="BAB84891.1"

/db_xref="GI:18676478"

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BASE COUNT 915 a 1642 c 1700 g 1034 t

ORIGIN

Alignment Scores:

Pred. No.:	Length:	Matches:	Conservative:	Mismatches:	Indels:	Gaps:
2.45e-22	5291	63	37	66	20	
Score:	293.00					
Percent Similarity:	53.76%					
Best Local Similarity:	33.87%					
Query Match:	29.24%					

US-09-895-298a-83 (1-190) x AK074065 (1-5291)

QY 1 MetMetasnpheglProProserlysAlaTPrArgAlaSerGlnMetMetThrPhePhe 20

DB 2057 CTGGCCAACTGCCAGCGCCGCCGCGCTGGCTCTACACATGACGACCGCTTCG 2116

QY 21 IlePheLeuLeuPhePheProSerPheThrGlyValLeuCyThrLeuAlaIleThrIle 40

DB 2117 CTCACGCTGCTGCTGCTCCCGCTTCCTGGCGCGCGCTGCTTCCTGCTACCGCGTC 2176

QY 41 TrpArgLeuLysProSerAlaAspCysGlyProPheArgGlyLeuProLeuPheIleHis 60

DB 2177 TGGCAGGTGAAGCCCTCGACACCTGCGGCCCTTCGACCCCTGACACATGTACGAG 2236

QY 61 SerIleTyrSerTrpIleAspThrLeu---SerThrArgProGlyTyrIleuTrpAlaVal 79

DB 2237 GCCGGCAGGCTGGTGGTGGCGCCTGAGGCGGCGGCGGCGCTCTCGTGGCTGCC 2296

QY 80 TrpIleTyrArgAsnLeuIleGlySerValHisPhePheIleuThrIleuLeuVal 99

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QY 140 LysLeuGlnAsp-----MetGlyLys 147
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QY 168 LeuGlyGlnHisAspGly 173
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BC004840 2848 bp mRNA linear ROD 07-AUG-2002
LOCUS BC004840 Mus musculus, similar to expressed in activated T/LAK lymphocytes,
ACCESSION BC004840 clone MGC:6819 IMAGE:2648849, mRNA, complete cds.
VERSION BC004840.1 GI:13436019
KEYWORDS MGC.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 2848)
REFERENCE
AUTHORS Strausberg, R.
TITLE Direct Submision
JOURNAL Submitted (21-MAR-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
REMARK NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT Contact: MGC help desk
Email: cgaabs-r@mail.nih.gov
Tissue Procurement: Lohar Hennighausen Ph.D., Chu-Xia Deng Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Baylor College of Medicine Human Genome
Sequencing Center
Center code: BCM-HGSC
Web site: http://www.hgsc.bcm.tmc.edu/cdna/
Contact: amgdbcm.tmc.edu
Gunnarhne, P.H., Garcia, A.M., Lu, X., Huilyk, S.W., Hale, S.M.,
Yoon, V.S., Kowis, C.R., Lawrence, S., Martin, R.G., Muzny, D.M.,
Richards, S., Gibbs, R.A.
Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Series: IRAX Plate: 5 Row: h Column: 13
This clone was selected for full length sequencing because it
passed the following selection criteria: Hexamer frequency ORF
analysis.
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VWVRLEHAGSGASWLPMLHFLVLENTFLPLASALLAVIYFNIOVVGQGRVYICLL
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BASE COUNT 533 a 828 c 836 g 651 t
ORIGIN
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Pred. No.: 1.64e-22 Length: 2848
Score: 291.50 Matches: 69
Percent Similarity: 54.87% Conservative: 38
Best Local Similarity: 35.38% Mismatches: 76
Query Match: 29.09% Indels: 12
DB: 10 Gaps: 4
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QY 41 TrpArgLeuLysProSerAlaAspCysGlyProPheArgGlyLeuProLeuPheIleHis 60
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